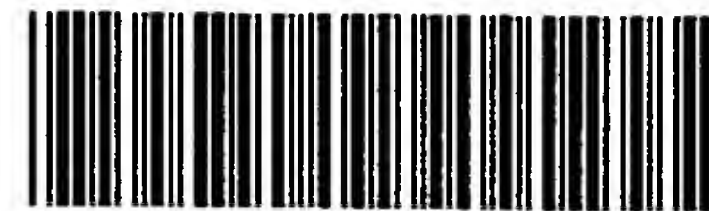


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591, 248
Source: IFWP
Date Processed by STIC: 09/12/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 09/12/2006

PATENT APPLICATION: US/10/591,248

TIME: 11:33:48

Input Set : A:\Q96497 Sequence Listing.txt

Output Set: N:\CRF4\09122006\J591248.raw

3 <110> APPLICANT: Kaneka Corp.
 4 OKUBO, Yuji
 5 MATSUMOTO, Keiji
 6 TAKAGI, Masamichi
 7 OHTA, Akinori
 9 <120> TITLE OF INVENTION: NOVEL TRANSFORMANT AND PROCESS FOR PRODUCING POLYESTER USING
 THE
 10 SAME
 12 <130> FILE REFERENCE: Q96497
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/591,248
 C--> 14 <141> CURRENT FILING DATE: 2006-08-31
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003589
 15 <151> PRIOR FILING DATE: 2005-03-03
 17 <150> PRIOR APPLICATION NUMBER: JP 2004-061291
 18 <151> PRIOR FILING DATE: 2004-03-04
 20 <150> PRIOR APPLICATION NUMBER: JP 2004-062812
 21 <151> PRIOR FILING DATE: 2004-03-05
 23 <160> NUMBER OF SEQ ID NOS: 39
 25 <170> SOFTWARE: PatentIn version 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 102
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: chemically-synthesized restriction enzyme cleavage site
 35 <400> SEQUENCE: 1
 36 aagctgcggc cgcagcttgc atgcctgcag gtcgactcta gaggatcctc gaggatcccc 60
 38 gggtacgcta gcgtaccgag ctatccattt aaatccgaat tc 102
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 1785
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: chemically-synthesized polynucleotide encoding mutant
 Aeromonas
 48 caviae phaC having mutation at codon 149
 50 <400> SEQUENCE: 2
 51 atgtctcaac catcttatgg tccattgttc gaagctttgg ctcatataca tgataaattg 60
 53 ttggctatgg ctaaagctca aaccgaaaga actgctcaag ccttggttgca aactaacttg 120
 55 gatgatttgg gtcaagtttt ggaacaaggt tctcaacaac catggcaatt gattcaagct 180
 57 caaatgaatt ggtggcaaga tcaattaaaa ttgatgcaac acactttggt aaaatctgct 240
 59 ggtcaaccat ctgaaccagt tattactcca gaaagatctg atagaagatt taaagctgaa 300
 61 gcttggtctg aacaaccaat ttatgattac ttaaaacaat cctatttggt aactgctaga 360
 63 catttggttg cttctgttga tgctttggaa ggtgtccac aaaaatctag agaaagattg 420

65 agattcttta ctagacaata cgtctccgct atggctccat ctaatttctt ggctactaac 480

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Input Set : A:\Q96497 Sequence Listing.txt

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67 ccagaattgt taaaattgac tttggaatcc gatggtcaaa atttggttag aggtttggct 540
69 ttattggctg aagatttgga aagatctgct gatcaattaa acattagatt gactgatgaa 600
71 tccgcttttg aattaggtag agatttggct ttgactccag gtagagttgt tcaaagaact 660
73 gaattatatg aattaattca atactctcca actactgaaa ccgttggtaa aaccccagtt 720
75 ttgatcggtc caccattcat taataaatat tacattatgg atatgagacc acaaaactcc 780
77 ttggtcgctt gggttggtcgc tcaagggtcaa accgttttca tgatttcctg gagaaacca 840
79 ggtggtgctc aagctcaa at tgatttagat gattatgttg ttgatgggtg cattgctgct 900
81 ttggatgggtg ttgaagccgc tactgggtgaa agagaagttc acggtattgg ttactgtatt 960
83 ggtgggtaccg ctttgtcttt agctatgggt tgggtggccg ccagaagaca aaaacaaaga 1020
85 gttagaactg ctactttggt tactactttg ttggatttct cccaaccagg tgaattgggt 1080
87 atttttattc atgaaccaat tatcgccgcc ttagaagccc aaaatgaagc taaaggtatt 1140
89 atggatggta gacaattggc cgtctccttc tctttgttga gagaaaactc tttatattgg 1200
91 aattactata ttgattctta cttaaaaggc caatctccag ttgcttttga tttgttgac 1260
93 tggaactctg attctactaa tgttgccggt aaaactcata actctttggt gagaagatta 1320
95 tatttggaaa atcaattggg taaagggtgaa ttaaaaatta gaaacactag aattgattta 1380
97 ggtaaagtta aaactccagt tttgttggtt tctgccgttg atgatcacat tgctttatgg 1440
99 caaggtacct ggcaagggtat gaaattgttc ggtgggtgaac aaagattttt attggccgaa 1500
101 tccggtcata ttgctggtat tattaatcca ccagctgcta acaaatacgg tttctggcac 1560
103 aatgggtgctg aagctgaatc tccagaatct tgggtggctg gtgccacca tcaagggtgg 1620
105 tcctggtggc cagaaatgat gggttttatt caaacagag atgaagggtc tgaaccagtc 1680
107 ccagccagag tcccagaaga aggtttggct ccagctccag gtcactatgt caaagttaga 1740
109 ttaaacccag ttttcgcttg tccaaccgaa gaagatgctg cttaa 1785

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112 <210> SEQ ID NO: 3

113 <211> LENGTH: 741

114 <212> TYPE: DNA

115 <213> ORGANISM: Artificial Sequence

117 <220> FEATURE:

118 <223> OTHER INFORMATION: chemically synthesized polynucleotide encoding *Ralstonia eutropha*

119 phbB for expression in *Candida maltosa*

121 <400> SEQUENCE: 3

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122 atgactcaaa gaattgccta cggtactggt ggtatgggtg gtattggtac tgctatttgt 60
124 caaagattgg ctaaagatgg ttttagagtt gttgctggtt gtgggtccaa ctctccaaga 120
126 agagaaaaat gggtggaaca acaaaaagct ttgggtttcg attttattgc ttctgaagg 180
128 aatgttgctg attgggattc tactaaaact gctttcgata aagtcaa atc cgaagtcggt 240
130 gaagttgatg ttttgattaa caatgctggt attactagag atgttggttt tagaaaaatg 300
132 actagagctg attgggatgc cggtattgat actaacttga cttctttggt caatgtcact 360
134 aaacaagtta ttgatgggtat ggctgataga ggttggggta gaattgtcaa catttcttct 420
136 gttaatggtc aaaaagggtc atttggtcaa actaactatt ccactgctaa agctgggtttg 480
138 catgggtttc ctatggcttt ggcccaagaa gttgccacta aagggtgttac tgtcaatacc 540
140 gtctctccag gttacattgc tactgatatg gtcaaagcca ttagacaaga tgttttagat 600
142 aaaattgtcg ccaccattcc agtcaaaaga ttgggtttgc cagaagaaat tgcttctatt 660
144 tgtgcttggt tgtcttctga agaatccggt ttttctactg gtgctgattt ctctttaaac 720
146 ggtgggtttgc acatgggtta a 741

```

149 <210> SEQ ID NO: 4

150 <211> LENGTH: 754

151 <212> TYPE: DNA

152 <213> ORGANISM: Artificial Sequence

154 <220> FEATURE:

155 <223> OTHER INFORMATION: chemically-synthesized promoter with multiple alkane responsible

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156         regions
158 <400> SEQUENCE: 4
159 aagcttgcat gcctgcaggt cgaaattcga gctcgggtacc cggggatcct ctagagtcca      60
161 tgtgcttttt tttttgtttt caatttgaaa gtttttttat ttccgcaata caaaattatt      120
163 ttttatccgc tcatgtgctt ttttttttgt tttcaatttg aaagtttttt tatttccgca      180
165 atacaaaatt attttttatc cgctgaccca gatcctctag agtccatgtg cttttttttt      240
167 tgttttcaat ttgaaagttt ttttatttcc gcaatacaaa attatttttt atccgctcat      300
169 gtgctttttt ttttgttttc aatttgaaag tttttttatt tccgcaatac aaaattattt      360
171 tttatccgct gaccagatc ctctagagtc catgtgcttt tttttttgtt ttcaatttga      420
173 aagttttttt atttccgcaa tacaaaatta ttttttatcc gctcatgtgc tttttttttt      480
175 gttttcaatt tgaaagttt tttatttccg caatacaaaa ttatttttta tccgctgacc      540
177 cagatctcga ctctagagga tccccgtttt tttatttccg caatacaaaa ttatttttta      600
179 tccgctttcc gttcctttct tcttgatgata aatctcaaca attatatata tcattccata      660
181 accctgaata attttttttt taagtccttg gtttcttttt ttagaaaaaa aggtgaatca      720
183 gtaaaatttt tgttatttat cattttaact caca                                754
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 594
188 <212> TYPE: PRT
189 <213> ORGANISM: Aeromonas caviae
191 <400> SEQUENCE: 5
193 Met Ser Gln Pro Ser Tyr Gly Pro Leu Phe Glu Ala Leu Ala His Tyr
194 1          5          10          15
197 Asn Asp Lys Leu Leu Ala Met Ala Lys Ala Gln Thr Glu Arg Thr Ala
198          20          25          30
201 Gln Ala Leu Leu Gln Thr Asn Leu Asp Asp Leu Gly Gln Val Leu Glu
202          35          40          45
205 Gln Gly Ser Gln Gln Pro Trp Gln Leu Ile Gln Ala Gln Met Asn Trp
206          50          55          60
209 Trp Gln Asp Gln Leu Lys Leu Met Gln His Thr Leu Leu Lys Ser Ala
210 65          70          75          80
213 Gly Gln Pro Ser Glu Pro Val Ile Thr Pro Glu Arg Ser Asp Arg Arg
214          85          90          95
217 Phe Lys Ala Glu Ala Trp Ser Glu Gln Pro Ile Tyr Asp Tyr Leu Lys
218          100         105         110
221 Gln Ser Tyr Leu Leu Thr Ala Arg His Leu Leu Ala Ser Val Asp Ala
222          115         120         125
225 Leu Glu Gly Val Pro Gln Lys Ser Arg Glu Arg Leu Arg Phe Phe Thr
226          130         135         140
229 Arg Gln Tyr Val Asn Ala Met Ala Pro Ser Asn Phe Leu Ala Thr Asn
230 145         150         155         160
233 Pro Glu Leu Leu Lys Leu Thr Leu Glu Ser Asp Gly Gln Asn Leu Val
234          165         170         175
237 Arg Gly Leu Ala Leu Leu Ala Glu Asp Leu Glu Arg Ser Ala Asp Gln
238          180         185         190
241 Leu Asn Ile Arg Leu Thr Asp Glu Ser Ala Phe Glu Leu Gly Arg Asp
242          195         200         205
245 Leu Ala Leu Thr Pro Gly Arg Val Val Gln Arg Thr Glu Leu Tyr Glu
246          210         215         220
249 Leu Ile Gln Tyr Ser Pro Thr Thr Glu Thr Val Gly Lys Thr Pro Val

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250 225          230          235          240
253 Leu Ile Val Pro Pro Phe Ile Asn Lys Tyr Tyr Ile Met Asp Met Arg
254          245          250          255
257 Pro Gln Asn Ser Leu Val Ala Trp Leu Val Ala Gln Gly Gln Thr Val
258          260          265          270
261 Phe Met Ile Ser Trp Arg Asn Pro Gly Val Ala Gln Ala Gln Ile Asp
262          275          280          285
265 Leu Asp Asp Tyr Val Val Asp Gly Val Ile Ala Ala Leu Asp Gly Val
266          290          295          300
269 Glu Ala Ala Thr Gly Glu Arg Glu Val His Gly Ile Gly Tyr Cys Ile
270 305          310          315          320
273 Gly Gly Thr Ala Leu Ser Leu Ala Met Gly Trp Leu Ala Ala Arg Arg
274          325          330          335
277 Gln Lys Gln Arg Val Arg Thr Ala Thr Leu Phe Thr Thr Leu Leu Asp
278          340          345          350
281 Phe Ser Gln Pro Gly Glu Leu Gly Ile Phe Ile His Glu Pro Ile Ile
282          355          360          365
285 Ala Ala Leu Glu Ala Gln Asn Glu Ala Lys Gly Ile Met Asp Gly Arg
286          370          375          380
289 Gln Leu Ala Val Ser Phe Ser Leu Leu Arg Glu Asn Ser Leu Tyr Trp
290 385          390          395          400
293 Asn Tyr Tyr Ile Asp Ser Tyr Leu Lys Gly Gln Ser Pro Val Ala Phe
294          405          410          415
297 Asp Leu Leu His Trp Asn Ser Asp Ser Thr Asn Val Ala Gly Lys Thr
298          420          425          430
301 His Asn Ser Leu Leu Arg Arg Leu Tyr Leu Glu Asn Gln Leu Val Lys
302          435          440          445
305 Gly Glu Leu Lys Ile Arg Asn Thr Arg Ile Asp Leu Gly Lys Val Lys
306          450          455          460
309 Thr Pro Val Leu Leu Val Ser Ala Val Asp Asp His Ile Ala Leu Trp
310 465          470          475          480
313 Gln Gly Thr Trp Gln Gly Met Lys Leu Phe Gly Gly Glu Gln Arg Phe
314          485          490          495
317 Leu Leu Ala Glu Ser Gly His Ile Ala Gly Ile Ile Asn Pro Pro Ala
318          500          505          510
321 Ala Asn Lys Tyr Gly Phe Trp His Asn Gly Ala Glu Ala Glu Ser Pro
322          515          520          525
325 Glu Ser Trp Leu Ala Gly Ala Thr His Gln Gly Gly Ser Trp Trp Pro
326          530          535          540
329 Glu Met Met Gly Phe Ile Gln Asn Arg Asp Glu Gly Ser Glu Pro Val
330 545          550          555          560
333 Pro Ala Arg Val Pro Glu Glu Gly Leu Ala Pro Ala Pro Gly His Tyr
334          565          570          575
337 Val Lys Val Arg Leu Asn Pro Val Phe Ala Cys Pro Thr Glu Glu Asp
338          580          585          590
341 Ala Ala
345 <210> SEQ ID NO: 6
346 <211> LENGTH: 246
347 <212> TYPE: PRT

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348 <213> ORGANISM: Ralstonia eutropha

350 <400> SEQUENCE: 6

352 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly

353 1 5 10 15

356 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala

357 20 25 30

360 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln

361 35 40 45

364 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp

365 50 55 60

368 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly

369 65 70 75 80

372 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val

373 85 90 95

376 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn

377 100 105 110

380 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala

381 115 120 125

384 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln

385 130 135 140

388 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu

389 145 150 155 160

392 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val

393 165 170 175

396 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys

397 180 185 190

400 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val

401 195 200 205

404 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu

405 210 215 220

408 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn

409 225 230 235 240

412 Gly Gly Leu His Met Gly

413 245

416 <210> SEQ ID NO: 7

417 <211> LENGTH: 2196

418 <212> TYPE: DNA

419 <213> ORGANISM: Artificial Sequence

421 <220> FEATURE:

422 <223> OTHER INFORMATION: chemically-synthesized ADE1 gene

424 <400> SEQUENCE: 7

425 taacagtatg attttttttcc ctctcccgtc gattgaggtt ttttttttct ctttcgtctt 60

427 ggtcttttgc ttttcactcc aaaaatggaa acacgcgcgg ctcaactcga aatccgtgat 120

429 caaaaaaata aaggctgtga gtttcgagcc aataattatg aattagtgggt attttttttta 180

431 aagataaata atcaagaatc gcattaggga gacgaatatg cgttattcaa ataaaaagac 240

433 aattcttttta gggtagcatt tcccttcaag ttcattccac atgtacatta atgtcaatga 300

435 tgtcgcagaa gttaaattag cagaagaaaa aaaaatgtg aattactccg agtcaactct 360

437 tctttctctt cttctttttc ttctttatca ccataatcac caccaccacc accaccacca 420

439 gctcccagat gacttcaact aacttagaag gaactttccc attgattgcc aaaggtaaag 480

VERIFICATION SUMMARY

DATE: 09/12/2006

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date